

In accordance with 37 CFR § 1.121, please substitute for original claims 1, 3, 10, 11, and 14, the following replacement versions of the same claims, as amended. The changes are shown explicitly in the attached "Marked Up Version Showing Changes Made."

C1 1. (Amended) A method of inducing apoptosis of a selected group of vertebrate cells *in vivo*, comprising administering to a vertebrate comprising said cells a thiaminase or derivative thereof or a non-pathogenic bacterium comprising a recombinant nucleic acid molecule encoding said thiaminase or derivative targeted to said selected group of vertebrate cells, thereby reducing the level of thiamin in said cells sufficiently to induce apoptosis of said cells.

C2 3. (Amended) A method for delivering a thiaminase or derivative thereof to vertebrate cells *in vivo*, comprising the step of contacting said cells with a non-pathogenic bacterium comprising a nucleic acid sequence encoding said thiaminase or derivative.

C3 10. (Amended) A eukaryotic expression vector comprising a recombinant nucleic acid sequence encoding a thiaminase.

C4 11. (Amended) A vector comprising a recombinant nucleic acid sequence encoding a thiaminase, wherein said thiaminase or derivative is different from a thiaminase from *Bacillus thiaminolyticus*.

C Please add the following new claims: 18.

C 18. (New) A purified, enriched, or isolated nucleic acid sequence encoding a thiaminase or derivative different from *Bacillus thiaminolyticus* thiaminase I, wherein said nucleic acid sequence is at least 70% identical to an equal length sequence at least 500 nucleotides in length of the *Naegleria gruberi* thiaminase sequence of SEQ ID NO. 3.

19. (New) The nucleic acid sequence of claim 18, wherein said nucleic acid sequence comprises a sequence at least 95% identical to the sequence of SEQ ID NO. 3.

20. (New) A method for identifying a nucleic acid sequence coding for a thiaminase from a species different from *Naegleria gruberi* or *Bacillus thiaminolyticus*, comprising identifying a nucleic acid sequence from said species that is homologous to a thiaminase sequence from *Naegleria gruberi* or *Bacillus thiaminolyticus*.

C4
C6+
21. (New) The method of claim 20, wherein said identifying comprises amplifying a nucleic acid sequence from said species using primers derived from *Naegleria gruberi* or *Bacillus thiaminolyticus*.

22. (New) The method of claim 20, wherein said identifying comprises performing sequence comparisons in a sequence database to identify homologous sequences.

23. (New) The method of claim 20, wherein said identifying comprises probing nucleic acid from said species with probes derived from *Naegleria gruberi* or *Bacillus thiaminolyticus*.

24. (New) The method of claim 20, wherein said identifying comprises sequencing at least a portion of a thiaminase sequence isolated from said species; and identifying a nucleic acid sequence from said species encoding said thiaminase sequence.

25. (New) A non-pathogenic bacterium encoding a recombinant nucleic acid sequence encoding a thiaminase.

26. (New) The bacterium of claim 25, wherein said bacterium is a *Clostridium* bacterium.

27. (New) The bacterium of claim 25, wherein said bacterium is a *Salmonella* bacterium.

28. (New) The method of claim 1, wherein said thiaminase is at least 35% identical to the thiaminase of SEQ ID NO: 4.

29. (New) The method of claim 1, wherein said thiaminase is at least 50% identical to the thiaminase of SEQ ID NO: 4.

30. (New) The method of claim 3, wherein said thiaminase is at least 35% identical to the thiaminase of SEQ ID NO: 4.

31. (New) The method of claim 3, wherein said thiaminase is at least 50% identical to the thiaminase of SEQ ID NO: 4.
